

Supplementary Materials

1 *Article*

2 **Epitope-Based Immunoinformatics Approach on** 3 **Nucleocapsid Protein of Severe Acute Respiratory** 4 **Syndrome-Coronavirus-2**

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22 **Table S1.** Scores from the combined B-cell linear epitope prediction.
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Method	Score		
	Maximum	Average	Minimum
BepiPred Linear Epitope Prediction	2.416	0.813	-0.001
Chou and Fasman Beta-Turn Prediction	1.439	1.070	0.610
Emini Surface Accessibility Prediction	7.006	1.000	0.050
Karplus and Schulz Flexibility Prediction	1.161	1.035	0.885
Kolaskar and Tongaonkar Antigenicity	1.197	0.988	0.874
Parker Hydrophilicity Prediction	6.871	2.800	-5.971

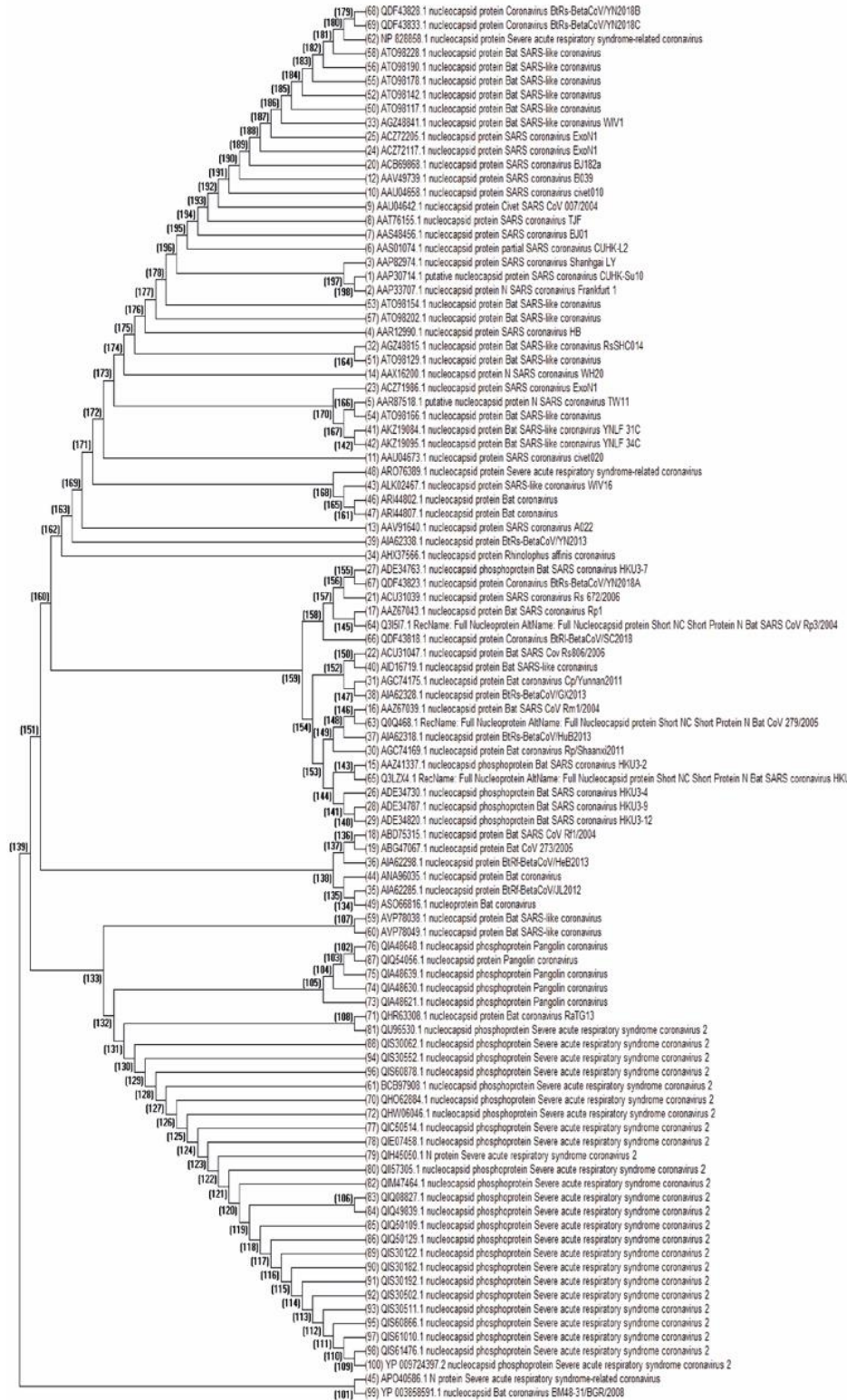
24 **Table S2.** Predicted B cell epitopes linear with the previous studies from Grifoni *et al.*, and Amrun *et al.*

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No.	Start	End	Peptide	Length
1	361	390	KTFPPTPEPKKDKKKKKADETQALPQRQKKQQ	30
2	52	59	WFTALTQH	8
3	154	166	NAAIVLQLPQGTT	13
4	347	363	KDQVILLNKHIDAYKTF	17
5	379	385	TQALPQR	7
6	389	401	QQTVTLLPAADLD	13
7	365	377	PTEPKKDKKKKAD	13
8	384	390	QRQKKQQ	7

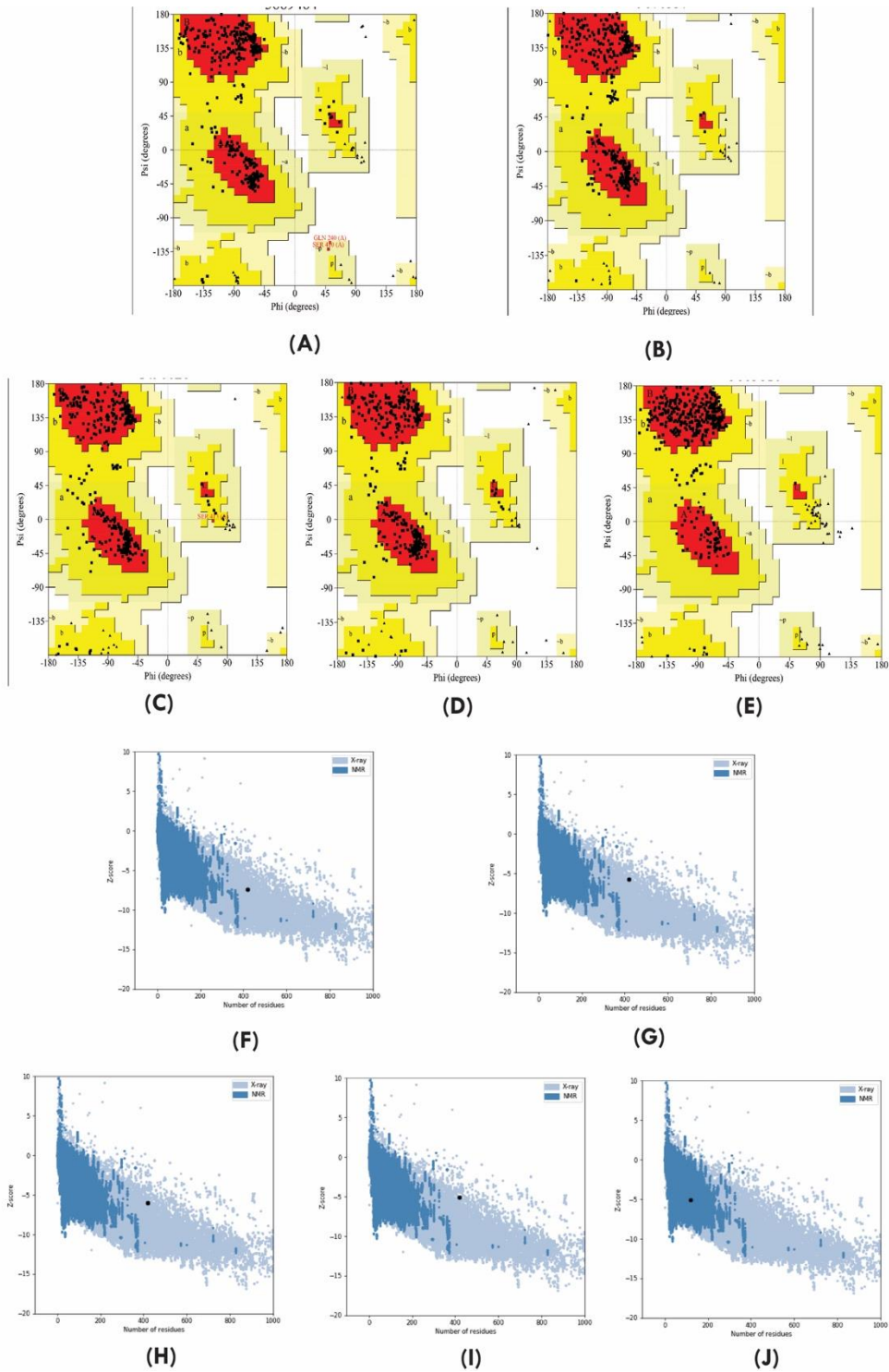
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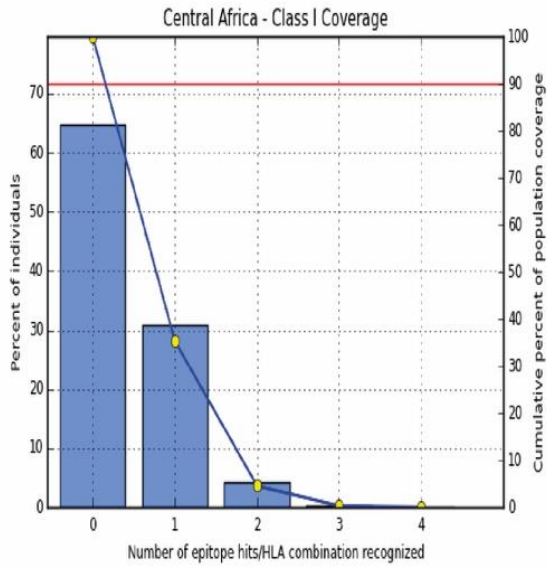
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29 **Figure S1:** Evolutionary divergence analysis of available N proteins of different strains; results are
 30 represented in a phylogenetic tree.

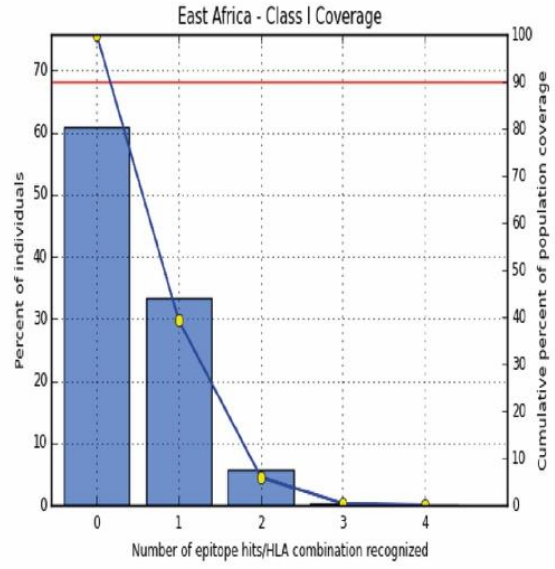


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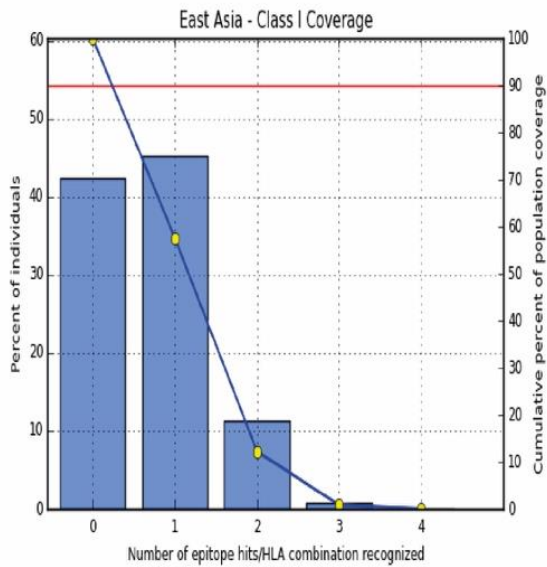
33 **Figure S2:** (A) Ramachandran plot analysis for model 1; (B) Ramachandran plot analysis for model 2; (C)
34 Ramachandran plot analysis for model 3; (D) Ramachandran plot analysis for model 5; (E)
35 Ramachandran plot analysis for the crystal structure of SARS-CoV-2 N protein (PDB ID; 6M3M); (F) Z-
36 score for model 1; (G) Z-score for model 2; (H) Z-score for model 3; (I) Z-score for model 5; (J) Z-score for
37 the crystal structure of SARS-CoV-2 N protein (PDB ID; 6M3M).



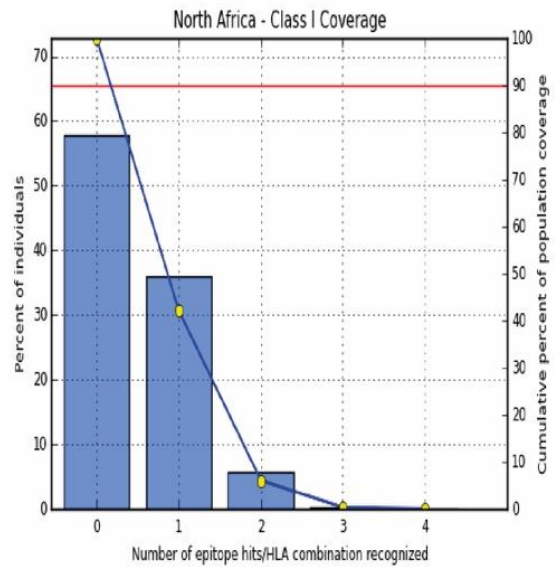
(A)



(B)



(C)

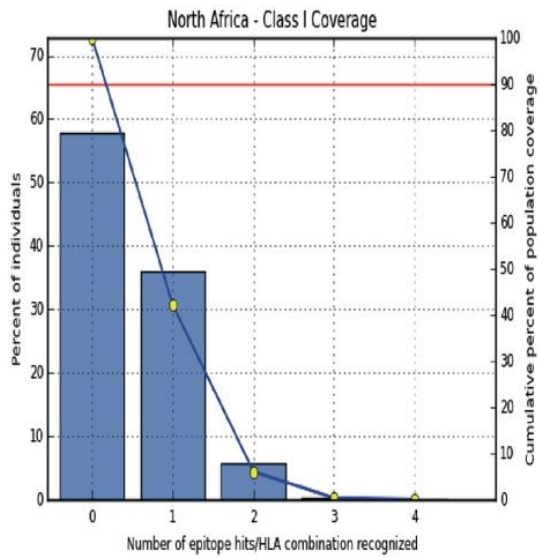


(D)

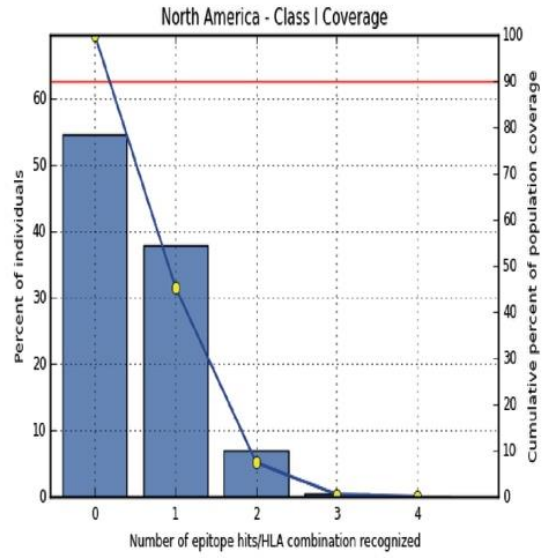
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40 **Figure S3:** Population coverage based on MHC restriction data for (A) Central Africa; (B) East Africa; (C)
 41 East Asia; (D) North Africa - using the Immune Epitope Database analysis resource.

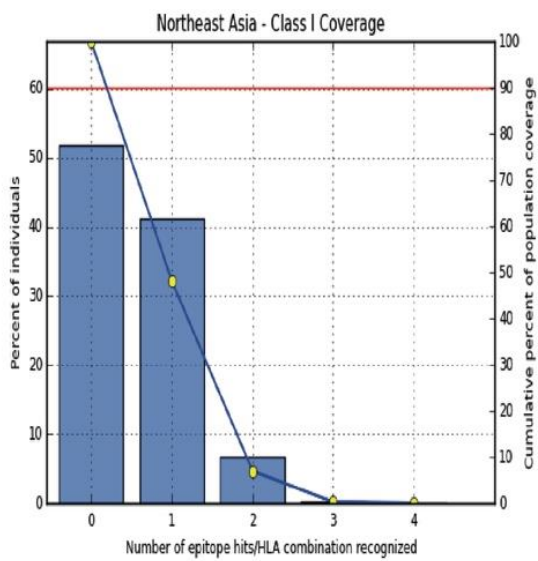
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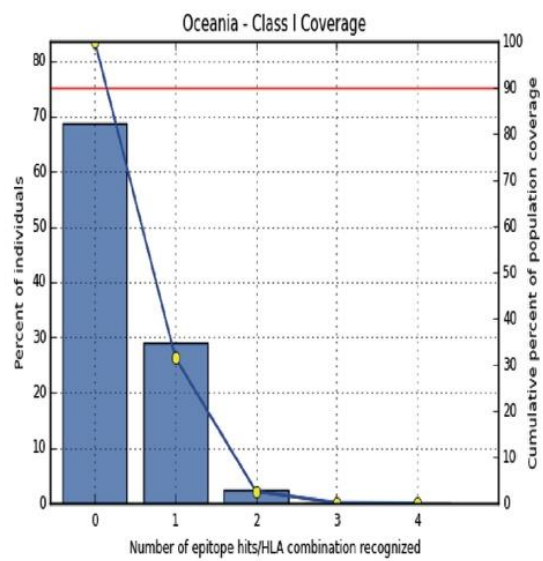
(A)



(B)



(C)



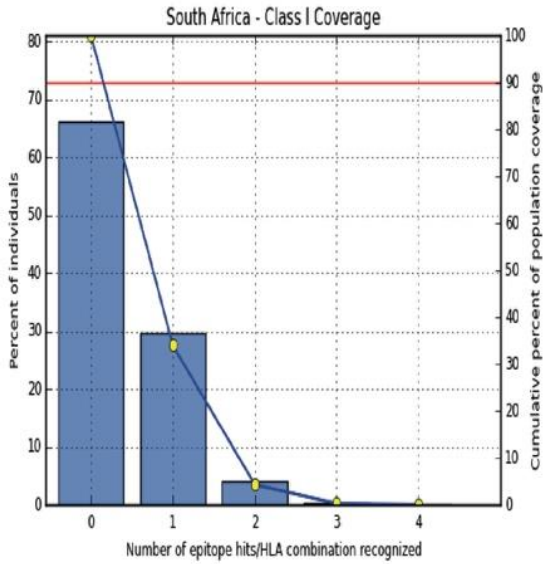
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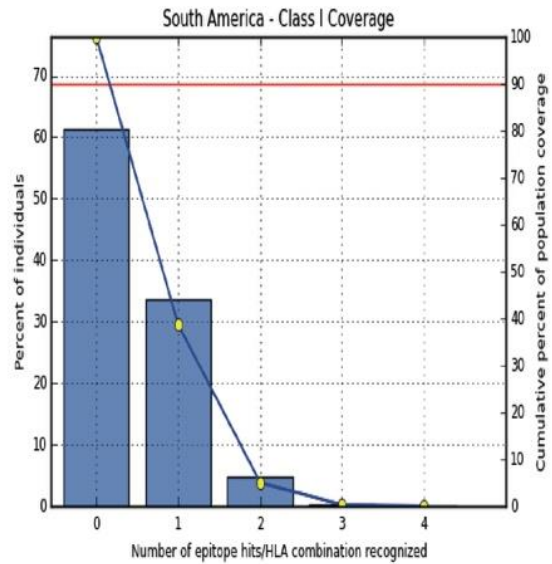
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45 **Figure S4:** Population coverage based on MHC restriction data for (A) North Africa; (B) North America;
 46 (C) Northeast Asia; (D) Oceania - using the Immune Epitope Database analysis resource.

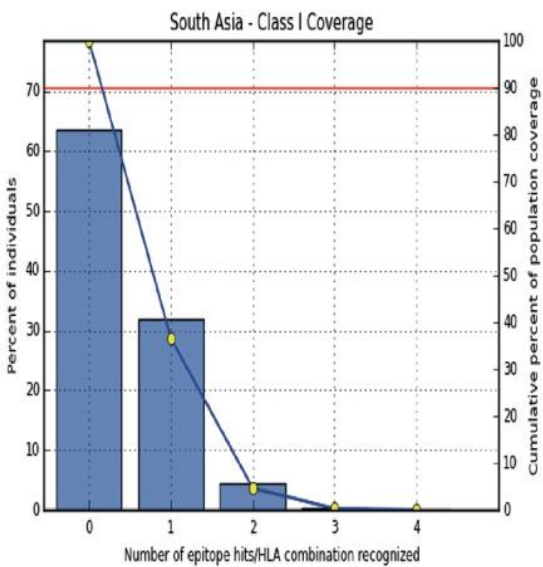
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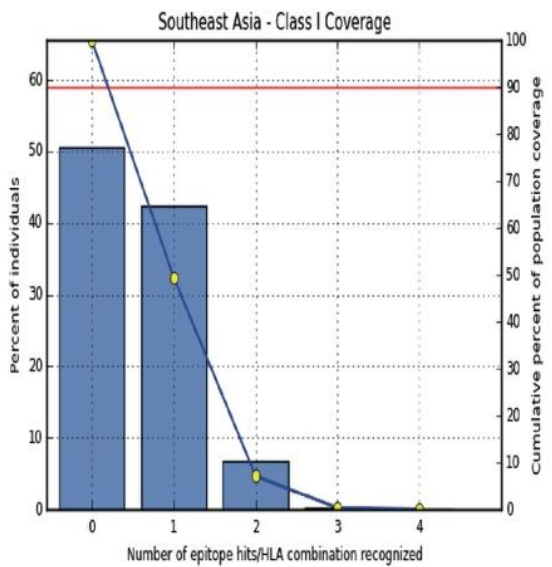
(A)



(B)



(C)



(D)

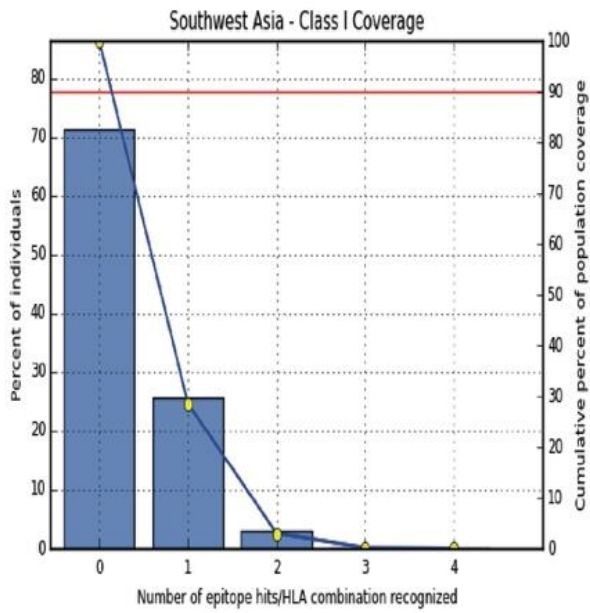
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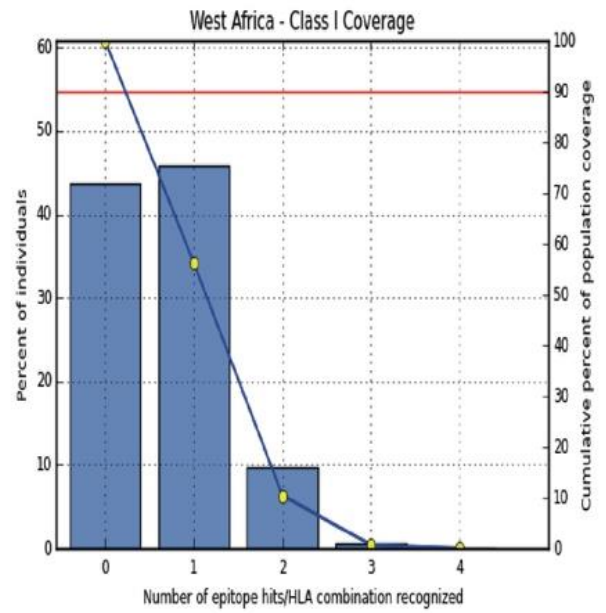
50 **Figure S5:** Population coverage based on MHC restriction data for (A) South Africa; (B) South America;

51 (C) South Asia; (D) Southeast Asia - using the Immune Epitope Database analysis resource.

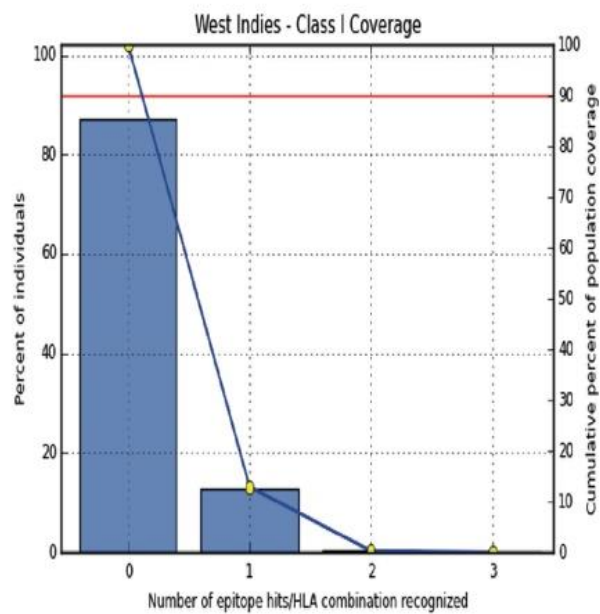
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(A)



(B)



(C)

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54 **Figure S6:** Population coverage based on MHC restriction data for (A) Southwest Asia; (B) West Africa;
 55 (C) West Indies - using the Immune Epitope Database analysis resource.

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